

RAW SEQUENCE LISTING

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Application Serial Number: 10/591,540
Source: IFWP
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IFWP

RAW SEQUENCE LISTING

DATE: 09/18/2006

PATENT APPLICATION: US/10/591,540

TIME: 15:20:32

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Output Set: N:\CRF4\09182006\J591540.raw

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3 <110> APPLICANT: Frohberg, Claus
4      Koetting, Oliver
5      Ritte, Gerhard
6      Steup, Martin
8 <120> TITLE OF INVENTION: Plants with reduced activity of multiple starch
phosphorylating enzymes
10 <130> FILE REFERENCE: 65084.000023
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/591,540
13 <141> CURRENT FILING DATE: 2006-09-01
15 <150> PRIOR APPLICATION NUMBER: EP04090088.8
16 <151> PRIOR FILING DATE: 2004-03-05
18 <150> PRIOR APPLICATION NUMBER: EP04090121.7
19 <151> PRIOR FILING DATE: 2004-03-29
21 <150> PRIOR APPLICATION NUMBER: US60/550,022
22 <151> PRIOR FILING DATE: 2004-03-05
24 <150> PRIOR APPLICATION NUMBER: EP04090203.3
25 <151> PRIOR FILING DATE: 2004-05-21
27 <150> PRIOR APPLICATION NUMBER: EP04090484.9
28 <151> PRIOR FILING DATE: 2004-12-09
30 <160> NUMBER OF SEQ ID NOS: 31
32 <170> SOFTWARE: PatentIn version 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 3591
36 <212> TYPE: DNA
37 <213> ORGANISM: Arabidopsis thaliana
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (1)..(3591)
42 <223> OTHER INFORMATION:
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50 act aga aac tca tca tca tca ctt cct aga ctc gtt aac atc act cac      96
51 Thr Arg Asn Ser Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His
52          20          25          30
54 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct      144
55 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser
56          35          40          45
58 cgt ctc act tgc act gct act tct tct tcc acc att gag gaa caa cgg      192
59 Arg Leu Thr Cys Thr Ala Thr Ser Ser Ser Thr Ile Glu Glu Gln Arg
60          50          55          60
62 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta      240
63 Lys Lys Lys Asp Gly Ser Gly Thr Lys Val Arg Leu Asn Val Arg Leu

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67	Asp	His	Gln	Val	Asn	Phe	Gly	Asp	His	Val	Ala	Met	Phe	Gly	Ser	Ala				
68					85					90				95						
70	aaa	gag	att	ggg	tca	tgg	aaa	aag	aaa	tcg	cct	ttg	aat	tgg	agt	gag	336			
71	Lys	Glu	Ile	Gly	Ser	Trp	Lys	Lys	Lys	Ser	Pro	Leu	Asn	Trp	Ser	Glu				
72				100					105					110						
74	aat	gga	tgg	gtt	tgt	gag	ttg	gaa	ctt	gac	ggg	ggg	cag	gtt	ttg	gag	384			
75	Asn	Gly	Trp	Val	Cys	Glu	Leu	Glu	Leu	Asp	Gly	Gly	Gln	Val	Leu	Glu				
76			115					120					125							
78	tat	aag	ttt	gtc	att	gtt	aag	aat	gat	ggg	tca	ctt	tca	tgg	gaa	tct	432			
79	Tyr	Lys	Phe	Val	Ile	Val	Lys	Asn	Asp	Gly	Ser	Leu	Ser	Trp	Glu	Ser				
80		130					135					140								
82	ggg	gat	aat	cgt	gtc	ctt	aag	gtt	cca	aat	tct	ggg	aat	ttt	tct	gtt	480			
83	Gly	Asp	Asn	Arg	Val	Leu	Lys	Val	Pro	Asn	Ser	Gly	Asn	Phe	Ser	Val				
84	145				150					155				160						
86	gtt	tgt	cat	tgg	gat	gct	act	aga	gaa	acc	ctt	gat	ttg	cct	cag	gag	528			
87	Val	Cys	His	Trp	Asp	Ala	Thr	Arg	Glu	Thr	Leu	Asp	Leu	Pro	Gln	Glu				
88				165					170				175							
90	gtt	ggg	aat	gat	gat	gat	gtt	ggg	gat	ggg	ggg	cat	gag	agg	gat	aat	576			
91	Val	Gly	Asn	Asp	Asp	Asp	Val	Gly	Asp	Gly	Gly	His	Glu	Arg	Asp	Asn				
92			180					185				190								
94	cat	gat	gtt	ggg	gat	gat	aga	gta	gtg	gga	agt	gaa	aat	ggg	gcg	cag	624			
95	His	Asp	Val	Gly	Asp	Asp	Arg	Val	Val	Gly	Ser	Glu	Asn	Gly	Ala	Gln				
96			195				200					205								
98	ctt	cag	aag	agt	aca	ttg	ggg	ggg	caa	tgg	caa	ggg	aaa	gat	gcg	tcc	672			
99	Leu	Gln	Lys	Ser	Thr	Leu	Gly	Gly	Gln	Trp	Gln	Gly	Lys	Asp	Ala	Ser				
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102	ttt	atg	cgt	tct	aat	gat	cat	ggg	aac	aga	gaa	gtt	ggg	aga	aat	tgg	720			
103	Phe	Met	Arg	Ser	Asn	Asp	His	Gly	Asn	Arg	Glu	Val	Gly	Arg	Asn	Trp				
104	225				230				235				240							
106	gat	act	agt	ggg	ctt	gaa	ggc	aca	gct	ctt	aag	atg	gtt	gag	ggg	gat	768			
107	Asp	Thr	Ser	Gly	Leu	Glu	Gly	Thr	Ala	Leu	Lys	Met	Val	Glu	Gly	Asp				
108				245				250				255								
110	cgc	aac	tct	aag	aac	tgg	tgg	aga	aag	ctt	gaa	atg	gta	cgc	gag	gtt	816			
111	Arg	Asn	Ser	Lys	Asn	Trp	Trp	Arg	Lys	Leu	Glu	Met	Val	Arg	Glu	Val				
112			260					265				270								

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130 cca gag gaa gtg ctt gtt gct cgg aaa atc cat ccg tgt tta cct tct      1056
131 Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser
132          340          345          350
134 ttc aaa gca gag ttt act gca gct gtc cct cta act cgg att agg gac      1104
135 Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp
136          355          360          365
138 ata gcc gat cgg aat gat att cct cat gat ctc aag caa gaa atc aag      1152
139 Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys
140          370          375          380
142 cat acg ata caa aat aag ctt cac cgg aat gct ggt cca gaa gat cta      1200
143 His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu
144 385          390          395          400
146 att gca aca gaa gca atg ctt caa cga att acc gag acc cca gga aaa      1248
147 Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys
148          405          410          415
150 tat agt gga gac ttt gtg gag cag ttt aaa ata ttc cat aat gag ctt      1296
151 Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu
152          420          425          430
154 aaa gat ttc ttt aat gct gga agt ctc act gaa cag ctt gat tct atg      1344
155 Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met
156          435          440          445
158 aaa att tct atg gat gat aga ggt ctt tct gcg ctc aat ttg ttt ttt      1392
159 Lys Ile Ser Met Asp Asp Arg Gly Leu Ser Ala Leu Asn Leu Phe Phe
160          450          455          460
162 gaa tgt aaa aag cgc ctt gac aca tca gga gaa tca agc aat gtt ttg      1440
163 Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu
164 465          470          475          480
166 gag ttg att aaa acc atg cat tct cta gct tct tta aga gaa aca att      1488
167 Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile
168          485          490          495
170 ata aag gaa ctt aat agc ggc ttg cga aat gat gct cct gat act gcc      1536
171 Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala
172          500          505          510
174 att gca atg cgc cag aag tgg cgc ctt tgt gag atc ggc ctc gag gac      1584
175 Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp
176          515          520          525
178 tac ttt ttt gtt cta cta agc aga ttc ctc aat gct ctt gaa act atg      1632
179 Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met
180          530          535          540
182 gga gga gct gat caa ctg gca aaa gat gtg gga tca aga aac gtt gcc      1680
183 Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala
184 545          550          555          560
186 tca tgg aat gat cca cta gat gct ttg gtg ttg ggt gtt cac caa gta      1728
187 Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val
188          565          570          575
190 ggt cta tct ggt tgg aag caa gaa gaa tgt tta gcc att gga aat gaa      1776
191 Gly Leu Ser Gly Trp Lys Gln Glu Cys Leu Ala Ile Gly Asn Glu
192          580          585          590
194 ctc ctt gct tgg cga gaa agg gac cta ctt gaa aaa gaa ggg gaa gag      1824

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195 Leu Leu Ala Trp Arg Glu Arg Asp Leu Leu Glu Lys Glu Gly Glu Glu
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198 gat gga aaa aca att tgg gcc atg agg ctg aaa gca act ctt gat cga      1872
199 Asp Gly Lys Thr Ile Trp Ala Met Arg Leu Lys Ala Thr Leu Asp Arg
200      610      615      620
202 gca cgc aga tta aca gca gaa tat tct gat ttg ctt ctt caa ata ttt      1920
203 Ala Arg Arg Leu Thr Ala Glu Tyr Ser Asp Leu Leu Leu Gln Ile Phe
204 625      630      635      640
206 cct cct aat gtg gag att tta gga aaa gct cta gga att cca gag aat      1968
207 Pro Pro Asn Val Glu Ile Leu Gly Lys Ala Leu Gly Ile Pro Glu Asn
208      645      650      655
210 agt gtc aag acc tat aca gaa gca gag att cgt gct gga att att ttc      2016
211 Ser Val Lys Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Ile Phe
212      660      665      670
214 cag atc tca aag ctc tgc act gtt ctt cta aaa gct gta aga aat tca      2064
215 Gln Ile Ser Lys Leu Cys Thr Val Leu Leu Lys Ala Val Arg Asn Ser
216      675      680      685
218 ctt ggt tct gag ggc tgg gat gtc gtt gta cct gga tgc acg tct ggg      2112
219 Leu Gly Ser Glu Gly Trp Asp Val Val Val Pro Gly Ser Thr Ser Gly
220      690      695      700
222 aca tta gtt cag gtt gag agc att gtt ccg gga tca ttg cca gca act      2160
223 Thr Leu Val Gln Val Glu Ser Ile Val Pro Gly Ser Leu Pro Ala Thr
224 705      710      715      720
226 tct ggt ggt cct att att ctc ttg gtc aat aaa gct gat ggc gat gaa      2208
227 Ser Gly Gly Pro Ile Ile Leu Leu Val Asn Lys Ala Asp Gly Asp Glu
228      725      730      735
230 gag gta agt gct gct aat ggg aac ata gct gga gtc atg ctt ctg cag      2256
231 Glu Val Ser Ala Ala Asn Gly Asn Ile Ala Gly Val Met Leu Leu Gln
232      740      745      750
234 gag ctg cct cac ttg tct cac ctt ggc gtt aga gcg cgg cag gag aaa      2304
235 Glu Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg Gln Glu Lys
236      755      760      765
238 att gtc ttt gtg aca tgt gat gat gat gac aag gtt gct gat ata cga      2352
239 Ile Val Phe Val Thr Cys Asp Asp Asp Asp Lys Val Ala Asp Ile Arg
240      770      775      780
242 cga ctt gtg gga aaa ttt gtg agg ttg gaa gca tct cca agt cat gtg      2400
243 Arg Leu Val Gly Lys Phe Val Arg Leu Glu Ala Ser Pro Ser His Val
244 785      790      795      800
246 aat ctg ata ctt tca act gag ggt agg agt cgc act tcc aaa tcc agt      2448
247 Asn Leu Ile Leu Ser Thr Glu Gly Arg Ser Arg Thr Ser Lys Ser Ser
248      805      810      815
250 gcg acc aaa aaa acg gat aag aac agc tta tct aag aaa aaa aca gat      2496
251 Ala Thr Lys Lys Thr Asp Lys Asn Ser Leu Ser Lys Lys Lys Thr Asp
252      820      825      830
254 aag aag agc tta tct atc gat gat gaa gaa tca aag cct ggt tcc tca      2544
255 Lys Lys Ser Leu Ser Ile Asp Asp Glu Glu Ser Lys Pro Gly Ser Ser
256      835      840      845
258 tct tcc aat agc ctc ctt tac tct tcc aag gat atc cct agt gga gga      2592
259 Ser Ser Asn Ser Leu Leu Tyr Ser Ser Lys Asp Ile Pro Ser Gly Gly

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266	gct gca tgt ggt ctt ctt gca tct tta gca gaa gcc tct agt aaa gtg			2688
267	Ala Ala Cys Gly Leu Leu Ala Ser Leu Ala Glu Ala Ser Ser Lys Val			
268		885	890	895
270	cac agc gaa cac gga gtt ccg gca tca ttt aag gtt cca act gga gtt			2736
271	His Ser Glu His Gly Val Pro Ala Ser Phe Lys Val Pro Thr Gly Val			
272		900	905	910
274	gtc ata cct ttt gga tcg atg gaa tta gct tta aag caa aat aat tcg			2784
275	Val Ile Pro Phe Gly Ser Met Glu Leu Ala Leu Lys Gln Asn Asn Ser			
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278	gaa gaa aag ttt gcg tct ttg cta gaa aaa cta gaa acc gcc aga cct			2832
279	Glu Glu Lys Phe Ala Ser Leu Leu Glu Lys Leu Glu Thr Ala Arg Pro			
280		930	935	940
282	gag ggt ggt gag cta gac gac ata tgt gac cag atc cat gaa gtg atg			2880
283	Glu Gly Gly Glu Leu Asp Asp Ile Cys Asp Gln Ile His Glu Val Met			
284	945	950	955	960
286	aaa acg ttg caa gtg cct aaa gaa aca atc aac agc ata agc aaa gcg			2928
287	Lys Thr Leu Gln Val Pro Lys Glu Thr Ile Asn Ser Ile Ser Lys Ala			
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290	ttt ctc aaa gat gct cgt ctc att gtt cgt tca agt gct aac gtc gag			2976
291	Phe Leu Lys Asp Ala Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu			
292		980	985	990
294	gac tta gcc gga atg tca gct gca gga ctc tat gaa tca atc cct aac			3024
295	Asp Leu Ala Gly Met Ser Ala Ala Gly Leu Tyr Glu Ser Ile Pro Asn			
296		995	1000	1005
298	gtg agt ccc tcg gat cct ttg gtg ttt tca gat tcg gtt tgc caa			3069
299	Val Ser Pro Ser Asp Pro Leu Val Phe Ser Asp Ser Val Cys Gln			
300		1010	1015	1020
302	gtt tgg gct tct ctc tac aca aga aga gct gtt cta agc cgt aga			3114
303	Val Trp Ala Ser Leu Tyr Thr Arg Arg Ala Val Leu Ser Arg Arg			
304		1025	1030	1035
306	gct gct ggt gtc tct caa aga gaa gct tca atg gct gtt ctc gtt			3159
307	Ala Ala Gly Val Ser Gln Arg Glu Ala Ser Met Ala Val Leu Val			
308		1040	1045	1050
310	caa gaa atg ctt tcg ccg gac tta tca ttc gtt ctg cac aca gtg			3204
311	Gln Glu Met Leu Ser Pro Asp Leu Ser Phe Val Leu His Thr Val			
312		1055	1060	1065
314	agt cca gct gat ccg gac agt aac ctt gtg gaa gcc gag atc gct			3249
315	Ser Pro Ala Asp Pro Asp Ser Asn Leu Val Glu Ala Glu Ile Ala			
316		1070	1075	1080
318	cct ggt tta ggt gag act tta gct tca gga aca aga gga aca cca			3294
319	Pro Gly Leu Gly Glu Thr Leu Ala Ser Gly Thr Arg Gly Thr Pro			
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322	tgg aga ctc gct tcg ggt aag ctc gac ggg att gta caa acc tta			3339
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VERIFICATION SUMMARY

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L:673 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:670
L:1364 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:1361